

Amendments to the specification:

On page 15, line 34, please replace the original paragraph with the following amended paragraph:

Figure 16 (SEQ ID NOS: 66 - 92) shows conservation between anchor regions of polypeptides of the invention.

On page 17, line 32, please replace the original paragraph with the following amended paragraph:

Escherichia coli

Polypeptides were found in pathogenic strains of *E. coli*, including enteropathogenic (EPEC), enteroaggregative (EAEC), enterohemorrhagic (EHEC) and uropathogenic (UPEC) strains. Furthermore, a polypeptide almost identical to those of the EHEC and EPEC strains was found in the K1 strain, which is a capsulated *E. coli* strain responsible for neonatal meningitis. The K1 sequence (SEQ ID NO: 93) aligns with NadA (SEQ ID NO: 94) as follows:

	100	110	120	130	140	150
k1.pep	TGVVQIPARYQSMINARQSAVTDAQOQTITEQQAQIVATQKTLAATGDTQNTAHYQEMIN					
				:: :: :: :: :: ::		
NadA.pep	DAALADTDAALDETTNALNKLGENITTFAEETKTNIWKIDEKLEAVADTVD--KHAEAFN					
	130	140	150	160	170	180
	160	170	180	190	200	210
k1.pep	ARLAAQNEANQRTTTEQGQKMNALTTDVAAQQOKERAQYDKQMQLAQKSVQAHEQIESL					
	: :: :::: : :: : :: : :: : :: : :: : ::					
NadA.pep	DIADSLDET--TKADEAVKTANEAKQTAEETKQNVDAKVKAAETAAGKAEAAAGTANTA					
	190	200	210	220	230	240
	220	230	240	250	260	270
k1.pep	RQDSAQTTQQLTNTQKRVADNSQQINTLNNHFDLSKNEVEDNRKEANAGTASAIASQP					
	: : : : :: : : : : : : : : : : : : ::					
NadA.pep	ADKAEAVAAKVTDIKADIATNKADIAKNSARIDSLDKNVANLRKETROGLAEQAALSGLF					
	250	260	270	280	290	300
	280	290	300	310	320	330
k1.pep	QVKTGDVMMVSAGAGTFNGESAVSVGTSFNAGTHTVLKAGISADTQSDFGAGVGVGYSF					
	: : : : : : : : : : : : : :					
NadA.pep	QPYNVGRFNVTAAVGGYKSESVAIAIGTGRFTENFAAKAGVAVGTSSGSSAAYHVGVNIEW					
	310	320	330	340	350	360

24.4% identity in 209 aa overlap

On page 20, line 1, please replace the original paragraph with the following amended paragraph:

Haemophilus

An incomplete NadA homolog was found in Brazilian purpuric fever (BPF) *Haemophilus influenzae* isolates {156}. This polypeptide has been named HadA. ~~NadA and HadA~~ HadA (SEQ ID NO: 95) and NadA (SEQ ID NO: 96) align as follows:

		10	20	30	40	
HadA. pep		MKRNLKQSVIAVLIGGTTVSNYALAAQAQAQVKKDELSELKKQVKEM-				
		:: :: : : :: :: : :				
NadA. pep	KTVNENKQNVDAKVKAAESEIEKLTTKLADTDAALADTDAALDETNTALNKLGENITTF					
	100 110 120 130 140 150					
	50 60 70 80 90 100					
HadA. pep	DAAIDGILDDNIAYEAEVDAKLDQHSAAALGRHTNRLNKLKTIAEKAKGDSSEALDKIEAL					
	: : : : : : : : : : :: : : : : : : :					
NadA. pep	EETKTNIVKIDEKLEAVADT-VDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEET					
	160 170 180 190 200 210					
	110 120 130 140 150 160					
HadA. pep	EEQNDEFLADITALEEGVDGLDDDIAGIQDNISD----IEDDINQNSADIATNTAAIATH					
	:: : : : : : : : : ::					
NadA. pep	KQNV D---AKVKAETAA-GKAEAAAGTANTAADKAEAVA AKVTDIKADIATNKADI AKN					
	220 230 240 250 260 270					
	170 180 190 200 210 220					
HadA. pep	TQRLDNLDNRVNNLNKDLKRGLAAQAALNGLFQPYNVGKLNLTAAVGGYKSTAVAVG					
	: :: :: : :					
NadA. pep	SARIDSLDKNVANLRKETRQGLAEQAALSGLFQPYNVGRFNVTA AVGGYKSES AVAIGTG					
	280 290 300 310 320 330					
NadA. pep	FRFTENFAAKAGVAVGTSSGSSAAYHVG VNYEW					
	340 350 360					

On page 21, line 5, please replace the original paragraph with the following amended paragraph:

~~NadA and the~~ The *H. actinomycescomitans* (SEQ ID NO: 97) and the NadA (SEQ ID NO: 98) sequence align as follows:

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10      20      30      40      50
actac.pe MTYQLFKHHLVALMVTGAISVNALAKDSFLENPSANLPQQVFKNR--VD--IFNNETNI
      |:: :|| :|:: || :|::|
NadA.pep TIYDIGEDGTITQKDATAADVEADDFKGLGLKKVVTNLTKTVNENKQNVDAKVKAASEEI
      60      70      80      90      100      110

      60      70      80      90      100      110
actac.pe NENKKDIAINKANIAASIEKDVMRNTGGIDRLAQELVNRARITKNELDIRKNTKSIAENT
      :: :| :| :|:: : : ::|:::|::: || : : | :| |::
NadA.pep EKLTTKLADTDAALADTDAALDETTNALNKLGEN-----ITTTAEETKTNIVKIDEKL
      120      130      140      150      160      170

      120      130      140      150      160
actac.pe ASIA-RIDGNLEGVNRVLQNVDRSTE-----NAARSRANE--QKIAENKKAIENKA
      ::| :| :| :| : ::| :| :| :| :| :| :| :| :| :| :| :| :|
NadA.pep EAVADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAETTKQNVDAKVKAETA
      180      190      200      210      220      230

      170      180      190      200      210      220
actac.pe DKADVEKNRADIAN-SRAIAT-FRSSQNIAALTTKVDRNTARIDRLDSRVNELDKVEK
      ||:: : :| :| :| :| :| : : : :| : : : :| :| :| :| :| :| :| :| :|
NadA.pep GKAEAAAGTANTAADKAEAAVAKVTDIKADIATNKAIAKNSARIDSLDKNVANLRKETR
      240      250      260      270      280      290

      230      240      250      260      270      280
actac.pe NGLASQAALSGLFQPYNVGSLNLSAAVGGYKSKTALAVGSGYRFNQNVAAKAGVAVSTN-
      :|| | | | | | | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
NadA.pep QGLAEQAALSGLFQPYNVGRFNVTAAVGGYKSESAVAIGTGFRFETENFAAKAGVAVGTSS
      300      310      320      330      340      350

      290
actac.pe GGSATYNVGLNFEW
      |::| :| :| :| :| :| :|
NadA.pep GSSAAYHGVGNYEW
      360

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37.0% identity in 284 aa overlap

On page 21, line 6, please replace the original paragraph with the following amended paragraph:

NadA and the The *H.somnus* (SEQ ID NO: 99) and the NadA (SEQ ID NO: 100) sequence align as follows:

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          90          100          110          120          130          140
H. somnus.pep EVIKGWNEVKSLPRIDGNGKDKQTKDQIAMLRITVDNTEKLGRIVSTNIEDIKNLKKELY
                                     | | | : : : : : | : |
NadA.pep      MSMKHFP SKVLTTAILATFCSGALAATSDD--DVKKAATVAIVAAYNNGQEIN
               10          20          30          40          50

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	150	160	170	180	190
H.somnus.pep	GF-----VEDVNES---EARNISRIDENEKDIKNL--KKELYDFVEDVNESEARNISRID				
	: :: : : : : :: : :::: :: :::				
NadA.pep	GFKAGETIYDIGEDGTITQKDATAADVEADDFKGLGLKKVVTNLTKTVNENKQNVDAKVK				
	60 70 80 90 100 110				
	200	210	220	230	240 250
H.somnus.pep	ENEKDINTLK-ELMDED--LNSVLTQIEDVKLTQDVNDNVNLAFFEEINGNAQKFDIAIE				
	:: : : : : : :::: : : : :: : : :				
NadA.pep	AAESEIEKLTTKLADTDAALADTDAALDETTNALNKLGENITTFAEETKTNIVKIDEKLE				
	120 130 140 150 160 170				
	260	270	280	290	300 310
H.somnus.pep	GLTSGLSDLQAKVDANKQETEDDIADNAKAIHSNTKGIKNTKDIRDLDTKTKQMLENDK				
	:::: : : : : : : :: : : : : : :				
NadA.pep	AVAD-----TVDKHA-EAFNDIADSLDETNTKADEAVKTANEAKQTAETKQ-----				
	180 190 200 210				
	320	330	340	350	360 370
H.somnus.pep	NLMTGLESLATETSKGFERFDVKTQQLDQAVANVVGVRVDITEQAIRQNTAGLVNVNKRVD				
	: : : : : : : : : : : : : : :				
NadA.pep	NVDAKVKAAETAAGKAEAAAAGTANTAADKAEA-VAKVTDIKADIATNKADIAKNSARID				
	220 230 240 250 260 270				
	380	390	400	410	420
H.somnus.pep	TLDKN-----TKAGIASAVALGMLPQSTAPGKSLVSLGVGHHRGQSATAIGVSSMSSN				
	: : : : : : : : : : : : : :				
NadA.pep	SLDKNVANLRKETROGLAEQAALSGLFQPNVGRFNVTAAGVGYKSESASAIG-TGFRFT				
	280 290 300 310 320 330				
	430	440	450		
H.somnus.pep	GKWVVKGGMSYDTQRHATFGGSGVGGFFN				
	: : : : : : : : : : : : : : : : : :				
NadA.pep	ENFAAKAGVAVGTSSGSSAAYHVGVNIEW				
	340 350 360				

23.2% identity in 354 aa overlap

On page 22, line 14, please replace the original paragraph with the following amended paragraph:

~~NadA and the~~ The *H. ducreyi* (SEQ ID NO: 101) and the NadA (SEQ ID NO: 102) sequence align
as follows:

	150	160	170	180	190	200
H.ducreyi.pe	SKNKQ	NIDTISKY	LLELGT	YLDG	SYRMMEQ	NTHNINKNTHNINKNTHNINKLSKELQTGL
				: : :: : : : :		
NadA.pep	EAAAGT	ANTAADKAE	AVAAKV	TDIKADI	ATNKADIAKNS	ARIDSLDKNVANLRKETRQGL
	240	250	260	270	280	290
	210	220	230	240	250	260
H.ducreyi.pe	ANQSALS	MVLVQP	NGVGKTS	VSAVGGY	RDKTALAIG	VGSRITDRFTAKAGVAFNTYNGG-
	: :	: : : :	: :	: :	: :	: : :
NadA.pep	AEQAALS	GGLFQ	PYNVGR	FNVTAAV	GGYKSES	AVAIGTGFRFTENFAAKAGVAVGTSSGSS
	300	310	320	330	340	350
	270					
H.ducreyi.pe	MSYGAS	VG	GYEF			
	: : : : :					
NadA.pep	AAYHVG	V	VNYEW			
	360					

47.5% identity in 101 aa overlap

An alignment of NadA and HadA (SEQ ID NO: 103) and NadA (SEQ ID NO: 104) (39.5% identity in 243 aa overlap) is given below:

[illegible]

On page 25, line 8 please replace the original paragraph with the following amended paragraph:

Immediately downstream of *hadA* is a gene encoding a hypothetical protein (SEQ ID NOS: 53 & 54), which is frame-shifted in strain KW20 and absent from all other *Haemophilus* strains tested. The closest database match for this protein is ZP_00132218. 1, the histone acetyltransferase HPA2 and related acetyltransferases from *Haemophilus somnus* 2336 (SEQ ID NO: 55):

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Length = 168

Score = 276 bits (707), Expect = 9e-74
Identities = 139/168 (82%), Positives = 149/168 (88%)

(SEQ ID NO: 105)
(SEQ ID NO: 106)
(SEQ ID NO: 107)

Query: 1 MINENLAYLSVLPLEDVKIERSSFSCSVEPLENYFHKYVSQDVKKGLAKCFVLINAQPSR 60
MINENL YLSVLPLED+ I+R+SFSCSVEPLE YF+KY SQDVKKG+ KCFVLIN Q
Sbjct: 1 MINENLPYLSVLPLEDLTIDRNSFSCSVEPLETYFYKYASQDVKKGITKCFVLINKQQFG 60

Query: 61 IVGYTSLALSIPIDIPQERISKGPYPNIPAVLIGRLAIDTNFQKQGYGKFLIADAIH 120
I+GYTSLALSIPIDIPQERISKG+PYPNIPAVL+GRLAIDTNFQ QGYGKFLIADAI+
Sbjct: 61 IIGYTTLSALSIPITDIPQERISKGIPYPNIPAVLVGRLAIDTNFQNGYGKFLIADAIY 120

Query: 121 KIKNATVAATILVVEAKNDASSFYERLGFIEFKEFGGTHRKLIFYPLT 168
KIKNATV A ILVVEAKND A SFY+RLGFIEFK THRKLIFYPLT
Sbjct: 121 KIKNATVGAAILVVEAKNDHAVSFYKRLGFIEFKNLKKTHRKLIFYPLT 168